STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

EFS

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: ___ 10/542,408D ___
Source: ___ TFWO ___
Date Processed by STIC: ___ 04/04/2007 ___

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
      http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/542,408 D_ .

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3_____Misaligned Amino Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4_____Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5_____Variable Length Sequence(s)_____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7_____Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8_____Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213> Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11_____Use of <220> Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12_____PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____ Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

RAW SEQUENCE LISTING   DATE: 04/04/2007
PATENT APPLICATION: US/10/542,408D   TIME: 14:54:46

Input Set : N:\efs\04_04_07\10542408D_efs\3136us0prevseq.txt
Output Set: N:\CRF4\04042007\J542408D.raw

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 3 <110> APPLICANT: ITO, Yasuaki
 4        FUJII, Ryo
 5        HINUMA, Shuji
 6        FUKUSUMI, Shoji
 7        MARUYAMA, Minoru
 9 <120> TITLE OF INVENTION: Novel Screening Method
11 <130> FILE REFERENCE: 3136 USOP
13 <140> CURRENT APPLICATION NUMBER: US 10/542408D
14 <141> CURRENT FILING DATE: 2005-07-15
16 <150> PRIOR APPLICATION NUMBER: JP 2003-010001
17 <151> PRIOR FILING DATE: 2003-01-17
19 <150> PRIOR APPLICATION NUMBER: JP 2003-104540
20 <151> PRIOR FILING DATE: 2003-04-08
22 <150> PRIOR APPLICATION NUMBER: JP 2003-194497
23 <151> PRIOR FILING DATE: 2003-07-09
25 <150> PRIOR APPLICATION NUMBER: JP 2003-329080
26 <151> PRIOR FILING DATE: 2003-09-19
28 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/000248
29 <151> PRIOR FILING DATE: 2004-01-15
31 <160> NUMBER OF SEQ ID NOS: 22
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 361
35 <212> TYPE: PRT
36 <213> ORGANISM: Homo sapiens
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40                   5                  10                  15
41 Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys
42                  20                  25                  30
43 Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val
44              35                  40                  45
45 Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
46          50                  55                  60
47 Val Ala Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn
48  65                  70                  75                  80
49 Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu
50                  85                  90                  95
51 Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His
52                 100                 105                 110
53 Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr
54             115                 120                 125
55 Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln
56         130                 135                 140
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57 Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala
58 145               150           155         160
59 Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe
60               165           170         175
61 Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser
62               180           185           190
63 Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp
64           195           200           205
65 Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
66       210           215           220
67 Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
68 225               230           235           240
69 Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
70               245           250           255
71 Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
72           260           265           270
73 Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
74           275           280           285
75 Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
76       290           295           300
77 Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
78 305               310           315           320
79 Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys
80               325           330           335
81 Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys
82           340           345           350
83 Arg Asn Asp Leu Ser Ile Ile Ser Gly
84       355           360
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87 <211> LENGTH: 1083
88 <212> TYPE: DNA
89 <213> ORGANISM: Homo sapiens
91 <400> SEQUENCE: 2
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93 aaccgcaccc gctttccctt cttctccgac gtcaagggcg accaccggct ggtgctggcc  120
94 gcggtggaga caaccgtgct ggtgctcatc tttgcagtgt cgctgctggg caacgtgtgc  180
95 gccctggtgc tggtggcgcg ccgacgacgc cgcggcgcga ctgcctgcct ggtactcaac  240
96 ctcttctgcg cggacctgct cttcatcagc gctatccctc tggtgctggc cgtgcgctgg  300
97 actgaggcct ggctgctggg ccccgttgcc tgccacctgc tcttctacgt gatgaccctg  360
98 agcggcagcg tcaccatcct cacgctggcc gcggtcagcc tggagcgcat ggtgtgcatc  420
99 gtgcacctgc agcgcggcgt gcggggtcct gggcggcggg cgcgggcagt gctgctggcg  480
100 ctcatctggg gctattcggc ggtcgccgct ctgcctctct gcgtcttctt ccgagtcgtc  540
101 ccgcaacggc tccccggcgc cgaccaggaa atttcgattt gcacactgat ttggcccacc  600
102 attcctggag agatctcgtg ggatgtctct tttgttactt tgaacttctt ggtgccagga  660
103 ctggtcattg tgatcagtta ctccaaaatt ttacagatca caaaggcatc aaggaagagg  720
104 ctcacggtaa gcctggccta ctcggagagc caccagatcc gcgtgtccca gcaggacttc  780
105 cggctcttcc gcaccctctt cctcctcatg gtctccttct tcatcatgtg gagccccatc  840
106 atcatcacca tcctcctcat cctgatccag aacttcaagc aagacctggt catctggccg  900
107 tccctcttct ctgggtggt ggccttcaca tttgctaatt cagccctaaa ccccatcctc  960
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RAW SEQUENCE LISTING   DATE: 04/04/2007
PATENT APPLICATION: US/10/542,408D   TIME: 14:54:46

Input Set : **N:\efs\04_04_07\10542408D_efs\3136us0prevseq.txt**
Output Set: **N:\CRF4\04042007\J542408D.raw**

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108 tacaacatga cactgtgcag gaatgagtgg aagaaaattt tttgctgctt ctggttccca 1020
109 gaaaagggag ccattttaac agacacatct gtcaaaagaa atgacttgtc gattatttct 1080
110 ggc                                                              1083
112 <210> SEQ ID NO: 3
113 <211> LENGTH: 361
114 <212> TYPE: PRT
115 <213> ORGANISM: Mus musculus
117 <400> SEQUENCE: 3
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119                  5                  10                  15
120 Leu Asp Gln Val Asn Arg Thr His Phe Pro Phe Phe Ser Asp Val Lys
121              20                  25                  30
122 Gly Asp His Arg Leu Val Leu Ser Val Val Glu Thr Thr Val Leu Gly
123          35                  40                  45
124 Leu Ile Phe Val Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
125      50                  55                  60
126 Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Ser Leu Val Leu Asn
127  65                  70                  75                  80
128 Leu Phe Cys Ala Asp Leu Leu Phe Thr Ser Ala Ile Pro Leu Val Leu
129                  85                  90                  95
130 Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Val Cys His
131              100                 105                 110
132 Leu Leu Phe Tyr Val Met Thr Met Ser Gly Ser Val Thr Ile Leu Thr
133          115                 120                 125
134 Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val Arg Leu Arg
135      130                 135                 140
136 Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala Ala Leu Leu Ala
137 145                 150                 155                 160
138 Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro Leu Cys Ile Leu
139                 165                 170                 175
140 Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp Gln Glu Ile Pro
141              180                 185                 190
142 Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu Ile Ser Trp Asp
143              195                 200                 205
144 Val Phe Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
145      210                 215                 220
146 Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
147 225                 230                 235                 240
148 Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
149                 245                 250                 255
150 Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
151              260                 265                 270
152 Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
153          275                 280                 285
154 Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
155      290                 295                 300
156 Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
157 305                 310                 315                 320
158 Tyr Asn Met Ser Leu Phe Arg Asn Glu Trp Arg Lys Ile Phe Cys Cys
```

```
159                  325               330               335
160 Phe Phe Phe Pro Glu Lys Gly Ala Ile Phe Thr Asp Thr Ser Val Arg
161              340               345               350
162 Arg Asn Asp Leu Ser Val Ile Ser Ser
163          355               360
165 <210> SEQ ID NO: 4
166 <211> LENGTH: 1083
167 <212> TYPE: DNA
168 <213> ORGANISM: Mus musculus
170 <400> SEQUENCE: 4
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172 aatcgcaccc acttcccttt cttctcggat gtcaagggcg accaccggtt ggtgttgagc  120
173 gtcgtggaga ccaccgttct ggggctcatc tttgtcgtct cactgctggg caacgtgtgt  180
174 gctctagtgc tggtggcgcg ccgtcggcgc cgtggggcga cagccagcct ggtgctcaac  240
175 ctcttctgcg cggatttgct cttcaccagc gccatccctc tagtgctcgt cgtgcgctgg  300
176 actgaggcct ggctgttggg gcccgtcgtc tgccacctgc tcttctacgt gatgacaatg  360
177 agcggcagcg tcacgatcct cacactggcc gcggtcagcc tggagcgcat ggtgtgcatc  420
178 gtgcgcctcc ggcgcggctt gagcggcccg gggcggcgga ctcaggcggc actgctggct  480
179 ttcatatggg gttactcggc gctcgccgcg ctgcccctct gcatcttgtt ccgcgtggtc  540
180 ccgcagcgcc ttcccggcgg ggaccaggaa attccgattt gcacattgga ttggcccaac  600
181 cgcataggag aaatctcatg ggatgtgttt tttgtgactt tgaacttcct ggtgccggga  660
182 ctggtcattg tgatcagtta ctccaaaatt ttacagatca cgaaagcatc gcggaagagg  720
183 cttacgctga gcttggcata ctctgagagc caccagatcc gagtgtccca acaagactac  780
184 cgactcttcc gcacgctctt cctgctcatg gtttccttct tcatcatgtg gagtcccatc  840
185 atcatcacca tcctcctcat cttgatccaa aacttccggc aggacctggt catctggcca  900
186 tcccttttct tctgggtggt ggccttcacg tttgccaact ctgccctaaa ccccatactg  960
187 tacaaacatgt cgctgttcag gaacgaatgg aggaagattt tttgctgctt cttttttcca 1020
188 gagaagggag ccatttttac agacacgtct gtcaggcgaa atgacttgtc tgttatttcc 1080
189 agc                                                            1083
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192 <211> LENGTH: 20
193 <212> TYPE: DNA
194 <213> ORGANISM: Artificial Sequence
196 <220> FEATURE:
197 <223> OTHER INFORMATION: primer
199 <400> SEQUENCE: 5
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203 <211> LENGTH: 20
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial Sequence
207 <220> FEATURE:
208 <223> OTHER INFORMATION: primer
210 <400> SEQUENCE: 6
211 cgctgtggat gtctatttgc                           20
213 <210> SEQ ID NO: 7
214 <211> LENGTH: 30
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
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RAW SEQUENCE LISTING   DATE: 04/04/2007
PATENT APPLICATION: **US/10/542,408D**   TIME: 14:54:46

Input Set : **N:\efs\04_04_07\10542408D_efs\3136us0prevseq.txt**
Output Set: **N:\CRF4\04042007\J542408D.raw**

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218 <220> FEATURE:
219 <223> OTHER INFORMATION: primer
221 <400> SEQUENCE: 7
222 agttcatttc cagtaccctc catcagtggc          30
224 <210> SEQ ID NO: 8
225 <211> LENGTH: 361
226 <212> TYPE: PRT
227 <213> ORGANISM: Rattus norvegicus
229 <400> SEQUENCE: 8
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231                   5                 10                  15
232 Pro Asp Gln Val Asn Arg Thr His Phe Pro Phe Phe Ser Asp Val Lys
233               20              25                  30
234 Gly Asp His Arg Leu Val Leu Ser Val Leu Glu Thr Thr Val Leu Gly
235           35              40              45
236 Leu Ile Phe Val Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
237       50                  55                  60
238 Val Val Arg Arg Arg Arg Arg Gly Ala Thr Val Ser Leu Val Leu Asn
239 65                  70              75                  80
240 Leu Phe Cys Ala Asp Leu Leu Phe Thr Ser Ala Ile Pro Leu Val Leu
241               85              90                  95
242 Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Val Cys His
243           100             105             110
244 Leu Leu Phe Tyr Val Met Thr Met Ser Gly Ser Val Thr Ile Leu Thr
245           115             120             125
246 Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val Arg Leu Arg
247       130             135             140
248 Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala Ala Leu Leu Ala
249 145             150             155             160
250 Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro Leu Cys Ile Leu
251               165             170             175
252 Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp Gln Glu Ile Pro
253           180             185             190
254 Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu Ile Ser Trp Asp
255           195             200             205
256 Val Phe Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
257       210             215             220
258 Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
259 225             230             235             240
260 Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
261               245             250             255
262 Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
263           260             265             270
264 Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
265           275             280             285
266 Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
267       290             295             300
268 Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
269 305             310             315             320
```

```
<210> 21
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<221> misc_RNA
<222> (20)..(21)
<223> n stands for deoxy thymidine

<400> 21
ggaccaggaa auuccgauun n                    21
```

If <213> Response is Artificial, pls Explain the Source of genetic material. See Item 11 on Error Summary Sheet.

't's are not allowed in RNA Sequence.

This Type of Error is in Seq ID 22

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/04/2007
PATENT APPLICATION: US/10/542,408D TIME: 14:54:48

Input Set : **N:\efs\04_04_07\10542408D_efs\3136us0prevseq.txt**
Output Set: **N:\CRF4\04042007\J542408D.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:21; N Pos. 20,21
Seq#:22; N Pos. 1,2

VERIFICATION SUMMARY   DATE: 04/04/2007
PATENT APPLICATION: US/10/542,408D   TIME: 14:54:48

Input Set : N:\efs\04_04_07\10542408D_efs\3136us0prevseq.txt
Output Set: N:\CRF4\04042007\J542408D.raw

L:435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0